## SEQUENCE LISTING

<110> Jin-Town Wang

Tzu-Lung Lin

<120> A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF

<160>5

<170>MICROSOFT WORD 2000

<210>SEQ ID NO:1

<211>LENGTH:5

<212>DNA

<213>ORGANISM: Helicobacter pylori

<400>SEQUENCE:1

ccatc 5

<210>SEQ ID NO:2

<211>LENGTH:1617

<212> DNA

<213> ORGANISM: Helicobacter pylori

<300>

<308>DDBJ/EMBL/Genbank; Accession No.: AB118944

<400> SEQUENCE:2

atg act aaa aaa aaa ccg gca cga aaa att tta agc ttt tca acc acc atg cga aac cct aaa 60
aga ata gga caa ttt tta gct gtt tta gga aag ttt gaa aat caa atc ctt aaa tct tca 120
ata atc atg caa att atc aaa tcc gtt ttg gct cat agg ctt tat aga cct act tct ctc 180
aat caa aat aaa gaa ttg aaa gaa ata tcc cca aaa ttt gac tcc aat gaa tat gtc ttt agc ggc ttt gag cat 300

360 gga gaa agc cgg ttt gac act tgg tat aag ctt atg tgt gag ttt ggt ttt 420 tat ata ctc atc agc gat agc gct aag atg ctt 480 tac aat gat gaa agc gta gaa aac gat gct ttt aaa gaa agc gtt gtt ggg gct ttt gga aac eet tae 540 tat gaa gta aaa aag aat aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa cga ctc aaa aat goo cat cta 600  $\infty$ gtc aaa gaa atc cct att tta ctt tgt tgg aaa gac gat aac gct 660 720 ctt tat gac tac att att cgt tta aga caa gaa atc gtt act atc aat aaa 780 ttt atc tat agc gat gaa gaa aaa tgc cta aaa ctt tta gaa agt gtt 840 ttt agc caa atc act aac gaa gcc gtt gat gaa tac att 900 att att att cgt ctt tca ttg cgt ggt aat ggt agg ttt gat att aat 960 aat aat gat tac att tta caa acc cat aag gct ttt ggg gat gac act ctc ttt gat 1020 aac gct aac aaa gcc ttt aac tac atg gcg atc gtg 1080 ctt act cca atc agc gct aat gag agc gtt aaa tca agc cta gca aac act tat act gat ttt aac aag 1140 aaa atc aag caa gaa tta ctc att act tgt caa gaa tca aaa gat agt ttt tta aga ctc att gat aaa cct tta tta 1200 att ttc ttg aaa caa cat ttt gaa aat tta 1260 agc agc gtg ata CCC aat tat agc gat ggc ttg cccgta tac aca gca agc ggt aat aaa cct gat att gta 1320 caa agt tat ata gaa gtg agc ttg att aga gac aga agt 1380 att goc aga cat tta 1440 ata cct aaa gaa ttg att aaa aat agc acc gtt ttt gta 1500 agt gct cca aat atc cat gat gat gcc aaa gaa 1560 gaa gcc caa ttc aaa gac aat att aat tgt tgt ata tat gct att aat aaa aaa gta gaa aac agc ata gaa tgg tta cag atc aat gac cat ttg aaa 1617

<210> SEQ ID NO:3

<211>LENGTH:538

<212>PRT

<213> ORGANISM: Helicobacter pylori

## <400>SEQUENCE:3

Met Thr Lys Lys Pro Ala Arg Lys Ile Leu Ser Phe Ser Thr Thr Met
1 5 10 15

Arg Asn Pro Lys Arg lle Gly Gln Phe Leu Ala Val Leu Gly Lys Phe Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys 55 Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met 90 Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu lle Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu 130 135 Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys 170 Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys 185 Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro 200 lle Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr 215 220 lle Arg Leu Arg Gln Glu lle Val Thr lle Asn Lys Thr Glu Phe 225 Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu 250 Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala 260 265 Val Asp Glu Tyr lie Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys lle Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu

305

310

Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile 325 330 330

Val Asp Ser Phe Leu Val Ser Val Thr Pro IIe Ser Ala Asn Glu Ser 340 345 350

Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp 355 360 365

Phe IIe Lys Gln Glu Leu Leu IIe Thr Cys Asn Lys Gln Glu Ser Lys 370 375 380

Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu 385 390 395 400

Ser Ala lle Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val lle Pro 405 410 415

Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly 420 425 430

Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gin Ser Tyr Ile
435 440 445

Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile 450 455 460

Pro lle Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile 465 470 485

Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala 485 490 495

Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys 500 505 510

Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu 515 520 525

Trp Leu Gln lle Asn Asp His Leu Lys Ala 530 535

<210>4

<211>780

<212> DNA

<213> ORGANISM: Helicobacter pylori

<300>

<308>DDBJ/EMBL/Genbank; Accession No.: AB118944

<400>4

atg ggg caa gac gct gat tit aaa gcg ctt gaa gaa ctg aaa gaa tac tit aat caa tta aag cta gaa gaa aat tat ttt agc caa cat ttt agc aac aag ttt 120 gat gtc atc ggt agc att aga gag cat ata gaa agc tta aac tta gat 180 tta aca agc ctg att tat tca atg gat aag ata 240 300 ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa gat aga ttt att ttt gag ctt aaa aat atc atg ata gag aga aaa aac gct 360 gct aaa acc tta gac tta gtc ttt att gat cct cca tac 420 aaa ata aat tca agg caa tac agc cgg ttt tat cat ctc tat gaa aac cta gtg cag tgg aaa aaa ccc aaa 480 agc gaa tat 540 aca gct tta aag cca tca tgc gag aac atg tgc cgc tct aat gcc aag aaa gaa agc gat tta att gaa aaa cta gat tgt aaa agg att gct tta 600 ggc ttt 660 acc tat aac tct aag tct agc tct tcg caa aat aaa ata aaa gat tta gga aaa tta agc gtt aaa gaa aag gct cat agt 720 gga aaa act gat ttt 780 aaa gag cat aaa gaa ttt tta ttt ata gtg gaa gtg aaa cct tga

<210>SEQ ID NO:5

<211>LENGTH:846

<212>DNA

<213> ORGANISM: Helicobacter pylori

<300>

<308>DDBJ/EMBL/Genbank; Accession No.: AB118944

## <400>SEQUENCE:5

atg cca caa ctc aat aag cta ttc cca aat aac att aat 60 gag cct 120 age gtg ttt tta ggt aac act aag gct aag aga tac tta gct aat gat atc cat aaa act tta agc aag ttc 180 aat gtt gag ctt 240 ggg att gaa ttg tct aaa att atc att cat tat ggc ttg tct ttc tct ttt aag gcc 300 tat ata aaa act tac tac gcc 360 tat cta agg gct gat ttt aac tcc aat caa aac aac atg ctt tat ttg ttg aat cac atg att aga ttt aat tct aaa ggg ctt 420

cct gtg ggt aat gtg gat ttc aat gaa aat gtt tat aat gcc cta aaa aac tac ata gat 480 ata cag caa aac acc att att tit cac aat gat gat tat att gat tit ctt aac cac 540 600 acc act tat tta aaa gat gat tat gtt tat ttt gac ccc cct tat tta atc tcc aat agt 660 gaa tac aac aag tta tgg gat agc gat aat gag ata gcc tta tat ggt gtt tta gat agc gat aaa aag gga gtt tta ttt ggt ata act aat ctt att tat cac aag gga gag act 720 att tta aaa gaa tgg gct aaa aaa tat tat att ttt aat atc aaa agt aat tat 780 atc agt tat aat gac aat act att aaa gaa gat agt caa gaa atc ttt gta act aat tat 840 846 agg tga